a) constructing a cDNA or genomic library of the DNA of said *C. elegans* cell or organism in a vector in an orientation relative to a promoter(s) that initiates transcription of said cDNA or DNA to double stranded (ds) RNA upon binding of a transcription factor to said promoter(s),

b) introducing said library into one or more of said *C. elegans* cells or organisms comprising said transcription factor, and

c) identifying a phenotype of said *C. elegans* cell or organism comprising said library and identifying the DNA or cDNA fragment from said library responsible for conferring said phenotype.

3.(twice amended) A method of assigning function to a known DNA sequence which method comprises

a) identifying a homologue(s) of said known DNA sequence in a *C. elegans* cell or organism,

b) isolating the relevant DNA homologue(s) or a fragment thereof from said *C. elegans* cell or organism,

c) cloning said homologue or fragment thereof into a vector in an orientation relative to a promoter(s) that initiates transcription of dsRNA from said DNA homologue or fragment upon binding of a transcription factor to said promoter(s),

d) introducing said vector into said *C. elegans* cell or organism from step a) comprising said transcription factor, and

e) identifying the phenotype of said *C. elegans* cell or organism compared to wild type.

12.(twice amended) A method according to claim 11 wherein said selectable marker comprises a nucleotide sequence capable of inhibiting or preventing expression of a gene in said *C. elegans* cell and which gene is responsible for conferring a phenotype.

14.(twice amended) A method according to claim 12 wherein said nucleotide sequence is a part of or identical to said gene sequence conferring said phenotype, and which nucleotide sequence is such as to permit integration of said vector by homologous recombination in the genome of

said *C. elegans* cell or organism and following said integration said nucleotide sequence is capable of inhibiting expression of said gene sequence conferring said phenotype.

20.(twice amended) A method according to any of claims 1 or 3 wherein said *C. elegans* cell or organism is contacted with a specified compound for screening for a desired phenotype.

38.(twice amended) A method of validating clones identified in yeast two hybrid vector experiments which method comprises

a) providing a construct including the DNA encoding the protein identified in the two hybrid vector experiment, which construct is such that said DNA is orientated relative to a promoter(s) that initiates transcription of said DNA to double stranded RNA upon binding of a transcription factor to said promoter(s),

b) transforming a *C. elegans* cell or organism comprising said transcription factor with said construct, and

c) identifying a phenotypic change in said *C. elegans* cell or organism when compared to a wild type.

92.(amended) A method according to claim 20 wherein said desired phenotype is resistance or sensitivity to said compound when compared to the wild type *C. elegans* cell or organism.

Remarks

Applicants have amended the claims to restrict the scope of the claims to the nematode *C. elegans*. No new matter has been added.

Rejections Under 35 U.S.C. § 112, First Paragraph

The Examiner maintained the rejection of claims 1-15, 17-21, 23, 24, 38-45 and 47-48, and rejected claim 92 under 35 U.S.C. § 112, first paragraph as not enabled. Applicants have amended the claims to limit the subject matter to the nematode *C. elegans*, and accordingly request reconsideration.

Applicants agree with the Examiner's recognition that the claims are enabled for the use of plasmid vector systems that initiate transcription of double stranded (ds) RNA. These are the